

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANTS: de la Monte, Suzanne
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
(B) STREET: 1100 New York Ave., Suite 600
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/380,203
(B) FILING DATE: 25-APR-2000
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US98/03685
(B) FILING DATE: 26-FEB-1998
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/038,908
(B) FILING DATE: 26-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Esmond, Robert W.
(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 0609.4370001
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-371-2600
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1442 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT	TGAG	ATG	GAG	TTT	TCG	CTC	TTG	TTG	CCC	AGG	CTG	GAG	TGC	50		
	Met	Glu	Phe	Ser	Leu	Leu	Leu	Pro	Arg	Leu	Glu	Cys				
	1				5					10						
AAT	GGC	GCA	ATC	TCA	GCT	CAC	GGG	AAC	CTC	CGC	CTC	CCG	GGT	TCA	AGC	98
Asn	Gly	Ala	Ile	Ser	Ala	His	Arg	Asn	Leu	Arg	Leu	Pro	Gly	Ser	Ser	
	15					20					25					
GAT	TCT	CCT	GCC	TCA	GCC	TCC	CCA	GTA	GCT	GGG	ATT	ACA	GGC	ATG	TGC	146
Asp	Ser	Pro	Ala	Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Gly	Met	Cys	
	30					35					40					
ACC	CAC	GCT	CGG	CTA	ATT	TTG	TAT	TTT	TTT	TTA	GTA	GAG	ATG	GAG	TTT	194
Thr	His	Ala	Arg	Leu	Ile	Leu	Tyr	Phe	Phe	Leu	Val	Glu	Met	Glu	Phe	
	45				50					55				60		
CTC	CAT	GTT	GGT	CAG	GCT	GGT	CTC	GAA	CTC	CCG	ACC	TCA	GAT	GAT	CCC	242
Leu	His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Pro	Thr	Ser	Asp	Asp	Pro	
				65				70						75		
TCC	GTC	TCG	GCC	TCC	CAA	AGT	GCT	AGA	TAC	AGG	ACT	GGC	CAC	CAT	GCC	290
Ser	Val	Ser	Ala	Ser	Gln	Ser	Ala	Arg	Tyr	Arg	Thr	Gly	His	His	Ala	
			80					85					90			
CGG	CTC	TGC	CTG	GCT	AAT	TTT	TGT	GGT	AGA	AAC	AGG	GTT	TCA	CTG	ATG	338
Arg	Leu	Cys	Leu	Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	
		95					100					105				
TGC	CCA	AGC	TGG	TCT	CCT	GAG	CTC	AAG	CAG	TCC	ACC	TGC	CTC	AGC	CTC	386
Cys	Pro	Ser	Trp	Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu	
	110					115					120					
CCA	AAG	TGC	TGG	GAT	TAC	AGG	CGT	GCA	GCC	GTG	CCT	GGC	CTT	TTT	ATT	434
Pro	Lys	Cys	Trp	Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile	
	125				130					135					140	
TTA	TTT	TTT	TTA	AGA	CAC	AGG	TGT	CCC	ACT	CTT	ACC	CAG	GAT	GAA	GTG	482
Leu	Phe	Phe	Leu	Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val	
				145					150					155		
CAG	TGG	TGT	GAT	CAC	AGC	TCA	CTG	CAG	CCT	TCA	ACT	CCT	GAG	ATC	AAG	530
Gln	Trp	Cys	Asp	His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	
			160					165						170		



CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTTA AACAGTTACA 1339
TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA 1399
GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA 1442

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
1 5 10 15
Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
20 25 30
Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
35 40 45
Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
50 55 60
Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
65 70 75 80
Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
85 90 95
Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
100 105 110
Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
115 120 125
Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
130 135 140
Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
145 150 155 160
His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
165 170 175
Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
180 185 190
Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
195 200 205

Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
210 215 220

Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
225 230 235 240

Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
245 250 255

Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
260 265 270

Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
275 280 285

Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
290 295 300

Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
305 310 315 320

Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
325 330 335

Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
340 345 350

Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
355 360 365

Ser Gln Thr Pro Asp Leu Arg
370 375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT	60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC	120
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTITAGTA	180
GAGATGGAGT TTAACCTCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC	240

TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC 300
 TGCCTGGCTA ATTTTTGTGG TAGAAACAGG GTTTCCTGA GTTTGCCCAA GCTGGTCTCC 360
 TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCCTCAGCC 420
 GTGCCTGGCC TTTTTATTTT ATTTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT 480
 GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC 540
 TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600
 TTTATTTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTACCCAG GCTGGAGTGC 660
 AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC 720
 CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTTGTAT 780
 TTTTAGTAGA GATGGGGTTT CACCATGTTC GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840
 GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCTGACT CCACGCCGGC 900
 CTATTTTTTAA TTTTGTGTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960
 AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC 1020
 AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT 1080
 CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AACTCCTGA CCTCAGGTGA 1140
 CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200
 GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
 TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320
 TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380
 C 1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCAGG CTGGAGTGCA ATGGCGCAAT 60

CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT 180
AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT 240
CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCC GCCTCTGCCT 300
GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT 360
CAAGCAGTCC ACCTGCCTCA GCCTCCCAAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC 420
TGGCCTTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT 480
GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC 540
TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTTAT 600
TTTTATTTTT AATTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG 660
GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCCAG 720
CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTTT TTGTATTTTT 780
AGTAGAGATG GGGTTTCACC ATGTTGCGCA GGTGATGCT AGATCTCTTG ACCTTGTGAT 840
CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC 900
TATTTTTAAT TTTTGTTTGT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA 960
ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT 1020
CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCGCTAA TTTTGTATT 1080
TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAACCTC TGACCTCAGG 1140
TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GCGGTGACGC CTCACCCAGC 1200
CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG 1260
GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACC AGCCAGTCAC 1320
ATTTTAAAC AGTTACATCT TTATTTTAGT AACTAGAAA GTGATACGAT AACATGGCGG 1380
AACCTGCAA TTCGAGTAGT ACAGAGTCTT TTATAACT 1418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear


(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- 
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14